

epo-FC-CIP-Jan2004.ST25
SEQUENCE LISTING

<110> Sun, Lee-Hwei K
Sun, Bill N
Sun, Cecily R

<120> Fc fusion proteins of human erythropoietin with high biological activities

<130> 02SUN2001-A

<140> to-be-assigned

<141> 2004-01-21

<150> 09/932812

<151> 2001-08-17

<160> 28

<170> PatentIn version 3.1

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<213> Artificial Sequence

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<223> PCR primer

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28

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 ttgtgtcga 69

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 gagtccaaat atggtccccc a 21

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<223> PCR primer

<400> 9

ggaattctca tttaccaga gacagga

28

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<211> 21

<212> DNA

<213> Artificial Sequence

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cctgagttcg cggggggacc a

21

<210> 11

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 11

gagtcctaat atggtcccc atgcccacca tgcccagcac ctgagttcgc ggggggacca

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<210> 12

<211> 70

<212> DNA

<213> Artificial Sequence

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<223> PCR primer

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tggtcccca 70

<210> 13

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<212> DNA

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<223> PCR primer

<400> 13

gacaaaactc acacatgccc a 21

<210> 14

<211> 23

<212> DNA

<213> Artificial sequence

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<223> PCR primer

<400> 14

acctgaagtc gcgggggggac cgt 23

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<212> DNA

<213> Artificial sequence

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<223> PCR primer

<400> 15

gacaaaactc acacatgccc accgtgccca gcacctgaag tcgcgggggg accgt 55

<210> 16

<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

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cacatgccca 70

<210> 17

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<212> DNA

<213> Artificial Sequence

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<223> HuEPO-L-VFc gamma2 (Figure 2A)

<400> 17

aagcttggcg cggagatggg ggtgcacgaa tgtcctgcct ggctgtggct tctcctgtcc 60

ctgctgtcgc tccctctggg cctcccagtc ctgggcgccc caccacgcct catctgtgac 120

agccgagtcc tggagaggta cctcttggag gccaaaggagg ccgagaatat cacgacgggc 180

tgtgtgaac actgcagctt gaatgagaat atcactgtcc cagacaccaa agttaatttc 240

tatgcctgga agaggatgga ggtcgggcag caggccgtag aagtctggca gggcctggcc 300

ctgctgtcgg aagctgtcct gcggggccag gccctgttgg tcaactcttc ccagccgtgg 360

gagcccctgc agctgcatgt ggataaagcc gtcagtggcc ttcgcagcct caccactctg 420

cttcgggctc tgggagccca gaaggaagcc atctcccctc cagatgcggc ctcagctgct 480

ccactccgaa caatcactgc tgacactttc cgaaaactct tccgagtcta ctccaatttc 540

ctccggggaa agctgaagct gtacacaggg gaggcctgca ggacagggga cggatccggt 600

ggcggttccg gtggaggcgg aagcggcggt ggaggatcag agcgcaaata ttgtgtcgag 660

tgcccaccgt gcccagcacc acctgtggca ggaccgtcag tcttcctctt cccccaaaa 720

cccaaggaca ccctcatgat ctcccgacc cctgagggtca cgtgcgtggg ggtggacgtg 780

agccacgaag accccgagggt ccagttcaac tgggtacgtgg acggcgtgga ggtgcataat 840

gccaagacaa agccacggga ggagcagttc aacagcacgt tccgtgtggg cagcgtcctc 900

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accgttgtgc accaggactg gctgaacggc aaggagtaca agtgcaaggt ctccaacaaa    960
ggcctcccag cctccatcga gaaaaccatc tccaaaacca aagggcagcc ccgagaacca    1020
caggtgtaca cctgcccccc atcccgggag gagatgacca agaaccaggt cagcctgacc    1080
tgcctggtca aaggcttcta ccccagcgac atcgccgtgg agtgggagag caatgggcag    1140
ccggagaaca actacaagac cacacctccc atgctggact ccgacggctc cttcttcctc    1200
tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcattgctcc    1260
gtgatgcatg aggcctctgca caaccactac acgcagaaga gcctctccct gtctccgggt    1320
aaatgagaat tc                                                         1332

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<210> 18

<211> 436

<212> PRT

<213> Artificial sequence

<220>

<223> HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure 2 A)

<400> 18

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Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1          5          10          15

```

```

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
20          25          30

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```

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
35          40          45

```

```

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
50          55          60

```

```

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
65          70          75          80

```

```

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
85          90          95

```

```

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
100         105         110

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Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
180 185 190

Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
195 200 205

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
210 215 220

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
225 230 235 240

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
245 250 255

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
260 265 270

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
275 280 285

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
290 295 300

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Ser
305 310 315 320

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
325 330 335

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
340 345 350

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
355 360 365

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Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
370 375 380

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
385 390 395 400

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
405 410 415

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
420 425 430

Ser Pro Gly Lys
435

<210> 19

<211> 1335

<212> DNA

<213> Artificial Sequence

<220>

<223> HuEPO-L-VFc gamma4 (Figure 2B)

<400> 19

aagcttggcg	cggagatggg	ggtgcacgaa	tgtcctgcct	ggctgtggct	tctcctgtcc	60
ctgctgtcgc	tccctctggg	cctcccagtc	ctgggcgccc	caccacgcct	catctgtgac	120
agccgagtcc	tggagaggta	cctcttggag	gccaaggagg	ccgagaatat	cacgacgggc	180
tgtgctgaac	actgcagctt	gaatgagaat	atcactgtcc	cagacaccaa	agttaatttc	240
tatgcctgga	agaggatgga	ggtcgggcag	caggccgtag	aagtctggca	gggcctggcc	300
ctgctgtcgg	aagctgtcct	gcggggccag	gccctgttgg	tcaactcttc	ccagccgtgg	360
gagcccctgc	agctgcatgt	ggataaagcc	gtcagtggcc	ttcgcagcct	caccactctg	420
cttcgggctc	tgggagccca	gaaggaagcc	atctcccctc	cagatgcggc	ctcagctgct	480
ccactccgaa	caatcactgc	tgacactttc	cgaaactct	tccgagtcta	ctccaatttc	540
ctccggggaa	agctgaagct	gtacacaggg	gaggcctgca	ggacagggga	cggatccggt	600
ggcggttccg	gtggaggcgg	aagcggcggt	ggaggatcag	agtccaaata	tgggtcccca	660
tgcccaccat	gcccagcacc	tgagttcgcg	gggggaccat	cagtcttcct	gttcccccca	720
aaaccaagg	acactctcat	gatctcccgg	accctgagg	tcacgtgcgt	ggtggtggac	780
gtgagccagg	aagaccccga	ggtccagttc	aactggtacg	tggatggcgt	ggaggtgcat	840

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```

aatgccaaga caaagccgcg ggaggagcag ttcaacagca cgtaccgtgt ggtcagcgtc   900
ctcaccgtcc tgcaccagga ctggctgaac ggcaaggagt acaagtgcaa ggtctccaac   960
aaaggcctcc cgtcctccat cgagaaaacc atctccaaag ccaaagggca gccccgagag  1020
ccacaggtgt acaccctgcc cccatcccag gaggagatga ccaagaacca ggtcagcctg  1080
acctgcctgg tcaaaggctt ctaccccagc gacatcgccg tggagtggga gagcaatggg  1140
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctctttcttc  1200
ctctacagca ggctaaccgt ggacaagagc aggtggcagg aggggaatgt cttctcatgc  1260
tccgtgatgc atgaggctct gcacaaccac tacacacaga agagcctctc cctgtctctg  1320
ggtaaagtag aattc                                     1335

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<210> 20

<211> 437

<212> PRT

<213> Artificial sequence

<220>

<223> HuEPO-L-VFc gamma4 with a 27-amino acid leader peptide (Figure 2B)

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Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
100 105 110

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Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
180 185 190

Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
195 200 205

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
210 215 220

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
225 230 235 240

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
245 250 255

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
260 265 270

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
275 280 285

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
290 295 300

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
305 310 315 320

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
325 330 335

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
340 345 350

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

355 epo-Fc-CIP-Jan2004.ST25 360 365

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
370 375 380

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
385 390 395 400

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
405 410 415

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
420 425 430

Leu Ser Leu Gly Lys
435

<210> 21

<211> 1329

<212> DNA

<213> Artificial Sequence

<220>

<223> HuEPO-L-VFc gamma1 (Figure 2C)

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agccgagtcc	tggagaggta	cctcttggag	gccaaaggagg	ccgagaatat	cacgacgggc	180
tgtgctgaac	actgcagctt	gaatgagaat	atcactgtcc	cagacaccaa	agttaatttc	240
tatgcctgga	agaggatgga	ggtcgggcag	caggccgtag	aagtctggca	gggcctggcc	300
ctgctgtcgg	aagctgtcct	gcggggccag	gccctgttgg	tcaactcttc	ccagccgtgg	360
gagcccctgc	agctgcatgt	ggataaagcc	gtcagtggcc	ttcgcagcct	caccactctg	420
cttcgggctc	tgggagccca	gaaggaagcc	atctcccctc	cagatgcggc	ctcagctgct	480
ccactccgaa	caatcactgc	tgacactttc	cgaaaactct	tccgagtcta	ctccaatttc	540
ctccggggaa	agctgaagct	gtacacaggg	gaggcctgca	ggacagggga	cggatccggt	600
ggcggttccg	gtggaggcgg	aagcggcggt	ggaggatcag	acaaaactca	cacatgccca	660
ccgtgcccag	cacctgaagt	cgcgggggga	ccgtcagtct	tcctcttccc	cccaaaaccc	720
aaggacaccc	tcatgatctc	ccggacacct	gaggtcacat	gcgtggtggt	ggacgtgagc	780

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aagacaaagc cgcgggagga gcagtacaac agcacgtacc gggtggtcag cgtcctcacc      900
gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggtctc caacaaagcc      960
ctcccagcct ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag     1020
gtgtacaccc tgcccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc     1080
ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg     1140
gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac     1200
agcaagctca ccgtggacaa gagcagggtg cagcagggga acgtcttctc atgctccgtg     1260
atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa     1320
tgagaattc                                     1329

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<210> 22

<211> 435

<212> PRT

<213> Artificial Sequence

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<223> HuEPO-L-VFc gamma1 with a 27-amino acid leader peptide (Figure 2C)

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Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
 100 105 110
 Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
 115 120 125
 Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
 130 135 140
 Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
 145 150 155 160
 Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
 165 170 175
 Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
 180 185 190
 Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 195 200 205
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Val Ala Gly
 210 215 220
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 225 230 235 240
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 245 250 255
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 260 265 270
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 275 280 285
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 290 295 300
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
 305 310 315 320
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 325 330 335
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 340 345 350

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Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
355 360 365

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
370 375 380

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
385 390 395 400

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
405 410 415

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
420 425 430

Pro Gly Lys
435

<210> 23

<211> 16

<212> PRT

<213> Artificial sequence, 16-amino acid peptide linker

<400> 23

Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 24

<211> 15

<212> PRT

<213> Human IgG1 hinge sequence

<400> 24

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 25

<211> 10

<212> PRT

<213> Truncated human IgG1 hinge sequence

<400> 25

Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10

<210> 26

<211> 232

<212> PRT

<213> Human IgG1 Fc with native hinge, CH2 and CH3 domains

<400> 26

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
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165

170

175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 27

<211> 228

<212> PRT

<213> Human IgG2 Fc with native hinge, CH2 and CH3 domains

<400> 27

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
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Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
20 25 30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
35 40 45

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
50 55 60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
65 70 75 80

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
85 90 95

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro
100 105 110

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
115 120 125

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Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
130 135 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145 150 155 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
165 170 175

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
195 200 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
210 215 220

Ser Pro Gly Lys
225

<210> 28

<211> 229

<212> PRT

<213> Human IgG4 Fc with native hinge, CH2 and CH3 domains

<400> 28

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

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Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser
			100					105					110		
Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro
		115					120					125			
Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln
	130					135					140				
Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala
145					150					155					160
Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr
				165					170					175	
Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu
			180					185					190		
Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser
		195					200					205			
Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser
	210					215					220				
Leu	Ser	Leu	Gly	Lys											
225															